Notification Date: July 20, 2022 Effective Date: August 23, 2022

Comprehensive Nephrology Gene Panel, Varies

Test ID: NEPHP

Useful for:

- Providing a genetic evaluation for patients with a personal or family history suggestive of hereditary kidney disease
- Establishing a diagnosis for a variety of hereditary kidney conditions including focal segmental
 glomerulosclerosis, nephritic/nephrotic syndrome, Alport syndrome, cystic kidney diseases (including
 polycystic kidney disease), nephronophthisis, tubulointerstitial disease, congenital anomalies of kidney and
 urinary tract, nephrocalcinosis, nephrolithiasis (kidney stones), renal electrolyte imbalances (including
 Bartter syndrome), C3 glomerulopathy, and complement-mediated thrombotic microangiopathy (also
 known as atypical hemolytic uremic syndrome)

Genetics Information:

This test utilizes next-generation sequencing to detect single nucleotide, deletion-insertion, and copy number variants in 302 genes associated with hereditary kidney disease: ABCC6, ACE, ACTN4, ADAMTS13, ADCY10, AGT, AGTR1, AGXT, AHI1, ALG1, ALG8, ALG9, ALMS1, ALPL, ANKS6, ANLN, ANOS1, APOA1, APOE, APOL1 [Chr22(GRCh37]:g.36661895-36661916 and g.36662023-36662062 only), APRT, AP2S1, AQP2, ARHGAP24, ARHGDIA, ARL13B, ARL6, ATP6V0A4, ATP6V1B1, ATP7B, AVP, AVPR2, B9D1, B9D2, BBIP1, BBS1, BBS10, BBS12, BBS2, BBS4, BBS5, BBS7, BBS9, BICC1, BSND, C2, C2CD3, C3, C5 [Chr9(GRCh37):g.123759950-123759973 only], C8A, C8orf37, CA2, CACNA1D, CACNA1H, CASR, CC2D2A, CD151, CD2AP, CD46 (MCP), CEP104, CEP120, CEP164, CEP290, CEP41, CEP83, CFB, CFH, CFHR1, CFHR2, CFHR3, CFHR4, CFHR5, CFI, CHD7, CLCN5, CLCNKA, CLCNKB, CLDN16, CLDN19, CNNM2, COL4A1, COL4A3, COL4A4, COL4A5, COL4A6, COQ2, COQ6, COQ8B, CPLANE1, CRB2, CREBBP, CSPP1, CTNS, CUBN, CUL3, CYP11B1, CYP11B2, CYP24A1, CYP27B1, CYP2R1, DCDC2, DDX59, DGKE, DHCR7. DMP1. DNAJB11. DYNC2H1. DZIP1L, EGF, EMP2, ENPP1, EYA1, FAH, FAM20A, FAN1, FAT1, FGA, FGF20, FGF23, FGFR1, FGFR2, FN1, FOXI1, FOXP1, FRAS1, FREM1, FREM2, FXYD2, GALNT3, GANAB, GATA3, GLA, GLI3, GLIS2, GNA11, GPC3, GREB1L, GRHPR, GRIP1, GSN, HNF1B, HNF4A, HOGA1, HPRT1, HPSE2, HSD11B2, IFT122, IFT140, IFT172, IFT27, IFT43, IFT80, IFT81, INF2, INPP5E, INVS, IQCB1, ITGA3, ITGA8, ITGB4, JAG1, KANK2, KCNA1, KCNJ1, KCNJ10, KCNJ5, KIAA0556 (KATNIP). KIAA0586, KIAA0753, KIF12, KIF14, KIF7, KL, KLHL3, LAMA5, LAMB2, LMNA, LMX1B, LRIG2, LRP2, LRP5, LYZ, LZTFL1, MAGED2, MAGI2, MAPKBP1, MEFV, MKKS, MKS1, MMACHC, MOCOS, MYH9, MYO1E, NEK1, NEK8, NLRP3, NOTCH2, NPHP1, NPHP3, NPHP4, NPHS1, NPHS2, NR3C2, NUP107, NUP133, NUP160, NUP205, NUP85, NUP93, OCRL, OFD1, PAX2, PBX1, PCBD1, PDE6D, PDSS2, PHEX, PKD1, PKD2, PKHD1, PLCE1, PLCG2, PLG, PMM2, PODXL, PRKCSH, PRPS1, PTPRO, REN, ROBO2, RPGRIP1L, SALL1, SALL4, SARS2, SCARB2, SCLT1, SCNN1A, SCNN1B, SCNN1G, SDCCAG8, SEC61A1, SEC63, SGPL1, SIX1, SLC12A1, SLC12A3, SLC17A5, SLC22A12, SLC26A1, SLC2A2, SLC2A9, SLC34A1, SLC34A3, SLC3A1, SLC4A1, SLC4A4, N27, SLC5A1, SLC5A2, SLC6A19, SLC7A7, SLC7A9, SLC9A3R1, SLIT2. SMARCAL1. TBC1D8B. TBX18. TCTN1. TCTN2. TCTN3. THBD. TMEM107. TMEM138. TMEM216. TMEM231, TMEM237, TMEM67, TRAF3IP1, TRIM32, TRPC6, TRPM6, TSC1, TSC2, TTC21B, TTC8, TTR, UMOD, VDR, VHL, VIPAS39, VPS33B, WDR19, WDR35, WDR72, WDR73, WNK1, WNK4, WNT4, WT1, XDH, XPNPEP3, ZMPSTE24, ZNF423.

Identification of a pathogenic variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for a variety of hereditary kidney diseases.

Methods:

Sequence Capture and Amplicon-Based Next Generation Sequencing (NGS)

Reference Values:

An interpretive report will be provided.

Ordering Guidance:

- Targeted testing for familial variants (also called site-specific or known mutations testing) is available for the genes on this panel. See FMTT / Familial Mutation, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.
- Customization of this panel and single gene analysis for any gene present on this panel are available. For more information, see CGPH / Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies.

Specimen Requirements:

Patient Preparation: A previous bone marrow transplant from an allogenic donor will interfere

with testing. Call 800-533-1710 for instructions for testing patients who

have received a bone marrow transplant.

Specimen Type: Whole blood

Preferred: Lavender top (EDTA) or yellow top (ACD)

Acceptable: Any anticoagulant

Specimen Volume: 3 mL

Collection Instructions: 1. Invert several times to mix blood.

2. Send whole blood specimen in original tube. Do not aliquot.

Specimen Stability Information: Ambient (preferred)/Refrigerated

Minimum Volume: 1 mL

Note:

Specimen preferred to arrive within 96 hours of collection.

Specimen Stability Information:

| Specimen Type | Temperature | Time | Special Container |
|---------------|-------------|------|-------------------|
| Varies | Varies | | |

Cautions:

Clinical Correlations:

- Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
- If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Detection of a reportable variant in an affected family member would allow for more informative testing of at-risk individuals.
- To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact the Mayo Clinic Laboratories genetic counselors at 800-533-1710.

Technical Limitations:

- Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or
 false-positive results may occur. The depth of coverage may be variable for some target regions; assay
 performance below the minimum acceptable criteria or for failed regions will be noted. Given these
 limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder
 is suspected, evaluation by alternative methods can be considered.
- This gene panel does **not** include assessment or interpretation of the common APOE alleles e2, e3, or e4.
- There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and
 duplication analysis as a result of technical limitations of the assay, including regions of homology, high
 guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be
 performed by alternate methodologies based on internal laboratory criteria.
- This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

Deletion/Duplication Analysis:

- This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon
 resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic
 complexity. Balanced structural rearrangements (such as translocations and inversions) may not be
 detected.
- This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline
 variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to
 clarify the significance of results.
- Genes may be added or removed based on updated clinical relevance. For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor.
- If the patient has had an allogeneic hematopoietic stem cell transplant or a recent blood transfusion, results
 may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for
 testing patients who have received a bone marrow transplant.

Reclassification of Variants:

At this time, it is not standard practice for the laboratory to systematically review previously classified
variants on a regular basis. The laboratory encourages healthcare providers to contact the laboratory at
any time to learn how the classification of a particular variant may have changed over time.

Variant Evaluation:

- Evaluation and categorization of variants are performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.(10) Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.
- Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools are interpreted with caution and professional clinical judgement.
- Rarely, incidental findings or secondary findings may implicate another predisposition or presence of active disease. Incidental findings may include, but are not limited to, results related to the sex chromosomes.
 These findings will be carefully reviewed to determine whether they will be reported.

CPT Code:

81401 x2

81404 x12

81405 x8

81406 x22

81407 x13

81408 x5

81479

Day(s) Performed: Varies Report Available: 28 to 42 days

Note:

The following referral test code(s) will become obsolete.

| Test Name | Test ID | Referral Lab Code | Referral Lab |
|---|---------|----------------------|---|
| Acrocallosal, Fetal Hydrolethalus, and Joubert Syndromes via the KIF7 Gene | ZW194 | 11031 | Prevention Genetics Lab |
| Apparent Mineralocorticoid Excess via the HSD11B2 Gene | ZW194 | 9969 | Prevention Genetics Lab |
| AQP2 (Nephrogenic Diabetes Insipidus) DNA Sequencing Test | ZW127 | 852 | Athena Diagnostics |
| Autosomal Dominant Pseudohypoaldosteronism Type 1 via the NR3C2 Gene | ZW194 | 11527 | Prevention Genetics Lab |
| Gitelman Syndrome via the SLC12A3 Gene | ZW194 | 4503 | Prevention Genetics Lab |
| Hypercalcemic and Hypocalcemic Disorders via the GNA11 Gene | ZW194 | 11359 | Prevention Genetics Lab |
| Hypophosphatasia via ALPL Gene Sequencing with CNV Detection | ZW194 | 7573 | Prevention Genetics Lab |
| Hypophosphatasia, infantile, childhood & adult types | ZW193 | 1565 | Connective Tissue Gene Tests Lab |
| Infantile Hypercalcemia | ZW199 | MML1197 | Nemours Children's Health- Molecular |
| JAG1 Gene Analysis in Alagille Syndrome Sequencing and Exon Array Dx of the entire gene NOW | ZW168 | 1004 | GeneDx, Inc. |
| Lesch-Nyhan Syndrome, HPRT-Related Hyperuricemia and Gout via the HPRT1 Gene | ZW194 | 7129 | Prevention Genetics Lab |
| Liddle Syndrome and Autosomal Recessive Pseudohypoaldosteronism Type 1 via the SCNN1B Gene | ZW194 | 11649 | Prevention Genetics Lab |
| Nail-Patella Syndrome via the LMX1B Gene | ZW194 | 8581 | Prevention Genetics Lab |
| Simpson-Golabi-Behmel Syndrome via GPC3 Gene | ZW194 | 9981 | Prevention Genetics Lab |
| Sotos Syndrome via the NSD1 Gene | ZW194 | 11529 | Prevention Genetics Lab |
| Complete PKDx Evaluation | ZW127 | 8100 | Athena Diagnostics |

| HNF1B Sequence Analysis | | 21961 | Baylor Medical Genetics Laboratories |
|--|-------|-------|---|
| Nephrolithiasis and Nephrocalcinosis Panel | | TH01 | GeneDx, Inc. |
| Autosomal Dominant and Recessive Polycystic Kidney Disease (ADPKD and ARPKD) Panel | | 10189 | Prevention Genetics Lab |
| Congenital Abnormalities of the Kidney and Urinary Tract (CAKUT) Panel | | 2667 | Prevention Genetics Lab |
| Focal Segmental Glomerulosclerosis (FSGS) via the ANLN Gene | | 91602 | Prevention Genetics Lab |
| Hereditary Cystic Kidney Diseases Panel | | 10619 | Prevention Genetics Lab |
| Nephrotic Syndrome (NS)/Focal Segmental Glomerulosclerosis (FSGS) Panel | ZW194 | 10417 | Prevention Genetics Lab |
| NPHP1 Deletion Test (Familial Juvenile Nephronophthisis) | ZW127 | 750 | Athena Diagnostics |
| Alport Syndrome NGS Panel Comprehensive | ZW193 | 5144 | Connective Tissue Gene Tests Lab |
| JAG1 Sequence Analysis | ZW221 | 3755 | Baylor medical Genetics Laboratories |
| LMX1B Comprehensive - Sequence and Deletion/Duplication Analysis | ZW221 | 7523 | Baylor medical Genetics Laboratories |
| OCRL Gene Sequencing | ZW168 | TA73 | GeneDx, Inc. |
| Alport Syndrome (AS) Panel | ZW194 | 10147 | Prevention Genetics Lab |
| Autosomal Dominant and Recessive Polycystic Kidney Disease (ADPKD and ARPKD) Panel | ZW194 | 10189 | Prevention Genetics Lab |
| Bartter Syndrome Type 1 via the SLC12A1 Gene | ZW194 | 11669 | Prevention Genetics Lab |
| Dent Disease Panel | ZW194 | 10077 | Prevention Genetics Lab |
| Distal Renal Tubular Acidosis Panel | | 10159 | Prevention Genetics Lab |
| Nephronophthisis and Joubert Syndrome via the NPHP1 Gene | | 15261 | Prevention Genetics Lab |
| Nephronophthisis and Senior-Loken Syndrome Sequencing Panel | | 10341 | Prevention Genetics Lab |
| Renal Hypomagnesemia 3 via the CLDN16 Gene | ZW194 | 8921 | Prevention Genetics Lab |

Questions

Contact Michelle Raths, Laboratory Technologist Resource Coordinator at 800-533-1710.